

Title: US-10-670-863-2  
 Perfect score: 1652  
 Sequence: 1 ctagtcgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 00:34:19 ; Search time 1168.87 Seconds  
 (without alignments)  
 9161.687 Million cell updates/sec

Title: US-10-670-863-2  
 Perfect score: 1652  
 Sequence: 1 ctagtcgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*  
 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*  
 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:57:24 ; Search time 7078.22 Seconds  
 (without alignments)  
 9527.774 Million cell updates/sec

Title: US-10-670-863-2  
 Perfect score: 1652  
 Sequence: 1 ctagtgcgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending Patents\_NA Main:\*

1: /cgn2\_6/ptodata/1/pna/PCTUS1\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/pna/PCTUS2\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/pna/PCTUS\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/pna/US07\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*  
 7: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*  
 8: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*  
 9: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*  
 10: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*  
 11: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*  
 12: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*  
 13: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq:\*  
 14: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq:\*  
 15: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq:\*  
 16: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq:\*  
 17: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq:\*  
 18: /cgn2\_6/ptodata/1/pna/US092A\_COMB.seq:\*  
 19: /cgn2\_6/ptodata/1/pna/US092B\_COMB.seq:\*

20: /cgn2\_6/ptodata/1/pna/US093A\_COMB.seq: \*  
21: /cgn2\_6/ptodata/1/pna/US093B\_COMB.seq: \*  
22: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq: \*  
23: /cgn2\_6/ptodata/1/pna/US095A\_COMB.seq: \*  
24: /cgn2\_6/ptodata/1/pna/US095B\_COMB.seq: \*  
25: /cgn2\_6/ptodata/1/pna/US095C\_COMB.seq: \*  
26: /cgn2\_6/ptodata/1/pna/US095D\_COMB.seq: \*  
27: /cgn2\_6/ptodata/1/pna/US096A\_COMB.seq: \*  
28: /cgn2\_6/ptodata/1/pna/US096B\_COMB.seq: \*  
29: /cgn2\_6/ptodata/1/pna/US096C\_COMB.seq: \*  
30: /cgn2\_6/ptodata/1/pna/US096D\_COMB.seq: \*  
31: /cgn2\_6/ptodata/1/pna/US096E\_COMB.seq: \*  
32: /cgn2\_6/ptodata/1/pna/US097A\_COMB.seq: \*  
33: /cgn2\_6/ptodata/1/pna/US097B\_COMB.seq: \*  
34: /cgn2\_6/ptodata/1/pna/US097C\_COMB.seq: \*  
35: /cgn2\_6/ptodata/1/pna/US098A\_COMB.seq: \*  
36: /cgn2\_6/ptodata/1/pna/US098B\_COMB.seq: \*  
37: /cgn2\_6/ptodata/1/pna/US098C\_COMB.seq: \*  
38: /cgn2\_6/ptodata/1/pna/US098D\_COMB.seq: \*  
39: /cgn2\_6/ptodata/1/pna/US099A\_COMB.seq: \*  
40: /cgn2\_6/ptodata/1/pna/US099B\_COMB.seq: \*  
41: /cgn2\_6/ptodata/1/pna/US099C\_COMB.seq: \*  
42: /cgn2\_6/ptodata/1/pna/US099D\_COMB.seq: \*  
43: /cgn2\_6/ptodata/1/pna/US099E\_COMB.seq: \*  
44: /cgn2\_6/ptodata/1/pna/US099F\_COMB.seq: \*  
45: /cgn2\_6/ptodata/1/pna/US099G\_COMB.seq: \*  
46: /cgn2\_6/ptodata/1/pna/US100A\_COMB.seq: \*  
47: /cgn2\_6/ptodata/1/pna/US100B\_COMB.seq: \*  
48: /cgn2\_6/ptodata/1/pna/US101A\_COMB.seq: \*  
49: /cgn2\_6/ptodata/1/pna/US101B\_COMB.seq: \*  
50: /cgn2\_6/ptodata/1/pna/US102A\_COMB.seq: \*  
51: /cgn2\_6/ptodata/1/pna/US102B\_COMB.seq: \*  
52: /cgn2\_6/ptodata/1/pna/US103A\_COMB.seq: \*  
53: /cgn2\_6/ptodata/1/pna/US103B\_COMB.seq: \*  
54: /cgn2\_6/ptodata/1/pna/US104A\_COMB.seq: \*  
55: /cgn2\_6/ptodata/1/pna/US104B\_COMB.seq: \*  
56: /cgn2\_6/ptodata/1/pna/US105A\_COMB.seq: \*  
57: /cgn2\_6/ptodata/1/pna/US105B\_COMB.seq: \*  
58: /cgn2\_6/ptodata/1/pna/US106A\_COMB.seq: \*  
59: /cgn2\_6/ptodata/1/pna/US107A\_COMB.seq: \*  
60: /cgn2\_6/ptodata/1/pna/US107B\_COMB.seq: \*  
61: /cgn2\_6/ptodata/1/pna/US107C\_COMB.seq: \*  
62: /cgn2\_6/ptodata/1/pna/US107D\_COMB.seq: \*  
63: /cgn2\_6/ptodata/1/pna/US108A\_COMB.seq: \*  
64: /cgn2\_6/ptodata/1/pna/US108B\_COMB.seq: \*  
65: /cgn2\_6/ptodata/1/pna/US109A\_COMB.seq: \*  
66: /cgn2\_6/ptodata/1/pna/US109B\_COMB.seq: \*  
67: /cgn2\_6/ptodata/1/pna/US109C\_COMB.seq: \*  
68: /cgn2\_6/ptodata/1/pna/US110\_COMB.seq: \*  
69: /cgn2\_6/ptodata/1/pna/US6000\_COMB.seq: \*  
70: /cgn2\_6/ptodata/1/pna/US6001\_COMB.seq: \*  
71: /cgn2\_6/ptodata/1/pna/US6002\_COMB.seq: \*  
72: /cgn2\_6/ptodata/1/pna/US6003\_COMB.seq: \*  
73: /cgn2\_6/ptodata/1/pna/US6004\_COMB.seq: \*  
74: /cgn2\_6/ptodata/1/pna/US6005\_COMB.seq: \*  
75: /cgn2\_6/ptodata/1/pna/US6006\_COMB.seq: \*  
76: /cgn2\_6/ptodata/1/pna/US6007\_COMB.seq: \*  
77: /cgn2\_6/ptodata/1/pna/US6008\_COMB.seq: \*  
78: /cgn2\_6/ptodata/1/pna/US6009\_COMB.seq: \*  
79: /cgn2\_6/ptodata/1/pna/US6010\_COMB.seq: \*  
80: /cgn2\_6/ptodata/1/pna/US6011\_COMB.seq: \*  
81: /cgn2\_6/ptodata/1/pna/US6012\_COMB.seq: \*  
82: /cgn2\_6/ptodata/1/pna/US6013\_COMB.seq: \*  
83: /cgn2\_6/ptodata/1/pna/US6014\_COMB.seq: \*  
84: /cgn2\_6/ptodata/1/pna/US6015\_COMB.seq: \*  
85: /cgn2\_6/ptodata/1/pna/US6016\_COMB.seq: \*  
86: /cgn2\_6/ptodata/1/pna/US6017\_COMB.seq: \*

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87: /cgn2_6/ptodata/1/pna/US6018_COMB.seq:*
88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq:*
89: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:*
90: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:*
91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
92: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq:*
93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq:*
94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq:*
95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq:*
97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq:*
98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq:*
100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq:*
101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq:*
102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq:*
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq:*
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq:*
106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq:*
108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
118: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
119: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
120: /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
121: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
122: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
123: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
124: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
127: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

```

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:38:19 ; Search time 2520.75 Seconds  
(without alignments)  
8309.150 Million cell updates/sec

Title: US-10-670-863-2  
Perfect score: 1652  
Sequence: 1 ctatgctgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 21945288 seqs, 6339366203 residues

Total number of hits satisfying chosen parameters: 43890576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq2:\*  
3: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq1:\*  
8: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
9: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq10:\*  
10: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:\*  
11: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq3:\*  
12: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq4:\*  
13: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq5:\*  
14: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq6:\*  
15: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq7:\*  
16: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq8:\*  
17: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq9:\*  
18: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq:\*  
19: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq2:\*  
20: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq3:\*  
21: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq4:\*  
22: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq5:\*  
23: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:22:19 ; Search time 189.213 Seconds  
(without alignments)  
9183.943 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_213\_1274  
Perfect score: 1062  
Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 00:34:19 ; Search time 751.415 Seconds  
(without alignments)  
9161.687 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_213\_1274  
Perfect score: 1062  
Sequence: 1 atgacagcaaagcctctaag.....tccgttatgggttctgtaag 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

'Total' number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:51:10 ; Search time 7408.62 Seconds  
(without alignments)  
10804.715 Million cell updates/sec

Title: US-10-670-863-2  
Perfect score: 1652  
Sequence: 1 ctatgctgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:38:50 ; Search time 959.585 Seconds  
(without alignments)

Title: US-10-670-863-2  
 Perfect score: 1652  
 Sequence: 1 ctatgcgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
 1: geneseqn1980s:\*  
 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 04:25:25 ; Search time 6009.98 Seconds  
 (without alignments)  
 10462.950 Million cell updates/sec

Title: US-10-670-863-2  
 Perfect score: 1652  
 Sequence: 1 ctatgcgacaactgagcaca.....ttaaaaaaaaaaaaaaaaaaa 1652

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est2:\*



3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:51:10 ; Search time 4762.68 Seconds  
(without alignments)  
10804.715 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_213\_1274  
Perfect score: 1062  
Sequence: 1 atgacagcaaagcctctaag.....tccgttatgggttctgtaag 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:38:50 ; Search time 616.876 Seconds  
(without alignments)  
10191.295 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_213\_1274  
Perfect score: 1062  
Sequence: 1 atgacagcaaagcctctaag.....tccgttatgggttctgtaag 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 04:25:25 ; Search time 3863.56 Seconds  
(without alignments)  
10462.950 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_213\_1274  
Perfect score: 1062  
Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*

8: gb\_gss1:\*  
9: gb\_gss2:\*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:51:10 ; Search time 4466.7 Seconds  
(without alignments)  
10804.715 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_279\_1274  
Perfect score: 996  
Sequence: 1 acaccagaaatctcatgcag.....tccgttatgggttctgtaag 996

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 02:38:50 ; Search time 578.539 Seconds  
(without alignments)  
10191.295 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_279\_1274  
Perfect score: 996  
Sequence: 1 acaccagaaatctcatgcag.....tccgttatgggttctgtaag 996

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 04:25:25 ; Search time 3623.45 Seconds  
(without alignments)  
10462.950 Million cell updates/sec

Title: US-10-670-863-2\_COPY\_279\_1274

Perfect score: 996

Sequence: 1 acaccagaaatctcatgcag.....tccgttatgggttctgtaag 996

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*